

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2003, 13:30:07 ; Search time 28.3382 Seconds
(without alignment)
2457.601 Million cell updates/sec

Title: US-09-807-933B-7
Perfect score: 1826
Sequence: 1 MKFTVAITSAVALALSSA.....TFKEVTCFALITRSGCERK 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 785.5 | 43.0 | 220 | 14 | Q9JH84 |
| 2 | 784.5 | 43.0 | 219 | 14 | Q9JH82 |
| 3 | 783.5 | 42.9 | 219 | 14 | Q9JH91 |
| 4 | 780.5 | 42.7 | 219 | 14 | Q9JH89 |
| 5 | 779.5 | 42.7 | 219 | 14 | Q9JH87 |
| 6 | 777.5 | 42.3 | 219 | 14 | Q9JH80 |
| 7 | 769.5 | 42.1 | 217 | 14 | Q9JH93 |
| 8 | 766.5 | 42.0 | 220 | 14 | Q9JH95 |
| 9 | 764.5 | 41.9 | 219 | 14 | Q9JH83 |
| 10 | 762.5 | 41.8 | 221 | 14 | Q9JH86 |
| 11 | 759.5 | 41.6 | 219 | 14 | Q9JH94 |
| 12 | 755.5 | 41.4 | 220 | 14 | Q9JH88 |
| 13 | 750.5 | 41.1 | 218 | 14 | Q9JH85 |
| 14 | 745.5 | 40.8 | 220 | 14 | Q9JH96 |
| 15 | 718 | 39.3 | 305 | 3 | Q93782 |
| 16 | 688 | 37.7 | 410 | 3 | Q9P868 |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 645 | 35.3 | 227 | 3 | Q93783 | Q93783 humicola gr |
| 18 | 560 | 30.7 | 242 | 5 | Q97401 | Q97401 phaenon coc |
| 19 | 559.5 | 30.6 | 271 | 3 | Q9UV93 | Q9UV93 alternaria |
| 20 | 383.5 | 21.0 | 112 | 14 | Q9JH99 | Q9JH99 unclassified |
| 21 | 371.5 | 20.3 | 112 | 14 | Q9JH98 | Q9JH98 unclassified |
| 22 | 371.5 | 20.3 | 112 | 14 | Q9JH92 | Q9JH92 unclassified |
| 23 | 368.5 | 20.2 | 112 | 14 | Q9JH90 | Q9JH90 unclassified |
| 24 | 365.5 | 20.0 | 112 | 14 | Q9JH91 | Q9JH91 unclassified |
| 25 | 350 | 19.2 | 111 | 14 | Q9JH97 | Q9JH97 unclassified |
| 26 | 269.5 | 14.8 | 476 | 3 | Q9C189 | Q9C189 humicola in |
| 27 | 233.5 | 12.8 | 471 | 3 | Q9HE78 | Q9HE78 trichoderma |
| 28 | 230 | 12.7 | 439 | 3 | Q92401 | Q92401 agaricus bi |
| 29 | 232 | 12.6 | 439 | 3 | Q9P893 | Q9P893 agaricus bi |
| 30 | 229.5 | 12.6 | 345 | 3 | Q9W217 | Q9W217 penicillium |
| 31 | 220.5 | 12.1 | 457 | 3 | Q93837 | Q93837 acromonium |
| 32 | 220.5 | 12.1 | 493 | 3 | Q9P8D0 | Q9P8D0 trichoderma |
| 33 | 205.5 | 11.3 | 408 | 3 | Q9HE22 | Q9HE22 phanerocha |
| 34 | 205 | 11.2 | 197 | 3 | Q9P7F1 | Q9P7F1 schizosach |
| 35 | 202.5 | 11.1 | 408 | 3 | Q9HE21 | Q9HE21 phanerocha |
| 36 | 199.5 | 10.9 | 444 | 3 | Q96VU2 | Q96VU2 lentinula e |
| 37 | 198 | 10.8 | 410 | 3 | Q12665 | Q12665 penicillium |
| 38 | 195 | 10.7 | 460 | 3 | Q02321 | Q02321 phanerocha |
| 39 | 194 | 10.6 | 443 | 3 | Q9C1R4 | Q9C1R4 lentinula e |
| 40 | 190.5 | 10.4 | 418 | 3 | Q93833 | Q93833 trichoderma |
| 41 | 182.5 | 10.0 | 823 | 3 | Q74203 | Q74203 phanerocha |
| 42 | 181.5 | 9.9 | 389 | 3 | Q9C3Z8 | Q9C3Z8 volvaria |
| 43 | 179.5 | 9.8 | 823 | 3 | Q9URP5 | Q9URP5 phanerocha |
| 44 | 177.5 | 9.7 | 802 | 3 | Q8TGC6 | Q8TGC6 phanerocha |
| 45 | 174.5 | 9.6 | 533 | 5 | Q9TY14 | Q9TY14 caenorhabdi |

ALIGNMENTS

RESULT 1
Q9JH84 PRELIMINARY; PRT; 220 AA.
ID Q9JH84
AC Q9JH84;
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohno K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045179; BAA98049.1; -.
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_P45; UNKNOWN 1.
SQ SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CRC64;

Query Match 43.0%; Score 785.5; DB 14; Length 220;
Best Local Similarity 66.7%; Pred. No. 1.3e-42;
Matches 136; Conservative 28; Mismatches 37; Indels 3; Gaps 2;
QY 136 SGGSTRVWDCCAKSGWPKASVNGPDTCAISNGISLIDAN--AOSGNGNGMPCNNQ 193
DB 17 SGRTRVWDCCAKSCAMEKKAATVPDTCCKDDITRIASNDTVKSSCDGDDGYCYOA 76
QY 194 PMAVNDELAYGFAAASIASAGNEAGMCCGCELTFTSGAASKKRVQVTTNGDLSNH 253
DB 77 PMAVNDSVAYGFAPAAACCG-GETGACCCNVCYELFTSGVNGKKRVQVTTNGDLSNQ 135
QY 254 DLMPGGGVGIFNGCAQMGAPNDGNGARVGVSSVSDCASLPSALQAGCKRRPWFNS 313
DB 136 DLMPGGGVGIVNGCTQSGAPADGWSRIVGVSSRSRSCQLPSGLQAGCOMRFDWFOA 195

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045176; BAA98046.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro: IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45.1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 23134 MW; 4BDEFAEC9ACC772D CRC64;

Query Match 42.7%; Score 779.5; DB 14; Length 219;
 Best Local Similarity 63.0%; Pred. No. 3.2e-42;
 Matches 133; Conservative 35; Mismatches 40; Indels 3; Gaps 2;

QY 129 ISGKSGSGSTTRVWDCCKASGWPGRASVTGPVDTCAASNGISLLDAN--AOSGCGANG 186
 DB 9 ISWLSADSGRTTRVWDCCKSGCGWEKKAANDKPIDTCAKQDTRVANSNDTVKSGCDGDDG 68
 QY 187 FMCNNNDPAVNDLAVGFAAASAGSNEAGWCCGCELTTSQAASKKRVVQVNTTGG 246
 DB 69 FMCQDQTPWQVSDLSYGFAPAAACCG-GEAGACCGCELTFTSPVNGKKRVVQVNTTGG 127
 QY 247 DLGSHFDLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCAALPDLQAGCKMR 306
 DB 128 DLGSHFDLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCAALPDLQAGCKMR 187
 QY 307 FMPKNSDNPMTFKEVTCPAELTTRSGCER 337
 DB 188 FDFWQNDNPISNFSQVSCPELIIAKTNCNR 218

RESULT 6
 Q9JH90 PRELIMINARY; PRT; 219 AA.
 AC Q9JH90;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045173; BAA98043.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro: IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45.1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 23037 MW; 372E016415530A9A CRC64;

Query Match 42.3%; Score 772.5; DB 14; Length 219;
 Best Local Similarity 63.7%; Pred. No. 8.8e-42;
 Matches 130; Conservative 32; Mismatches 39; Indels 3; Gaps 2;
 QY 136 SGSTTRVWDCCKASGWPGRASVTGPVDTCAASNGISLLDAN--AOSGCGANGFMCNNNQ 193
 DB 16 SGTTRVWDCCKSGCGWEKKAANDKPIDTCAKQDTRVANSNDTVKSGCDGDFMCYDQT 75
 QY 194 PMAVNDLAVGFAAASAGSNEAGWCCGCELTTSQAASKKRVVQVNTTGGDLGSHNF 253

DB 76 PMQVSDLSYGFAPAAACCG-GEAGACCGCELTFTSPVNGKKRVVQVNTTGGDLGSHNF 134
 QY 254 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCAALPDLQAGCKMRFMPKNS 313
 DB 135 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCAALPDLQAGCKMRFMPKNS 194
 QY 314 DNPTMTFKEVTCPAELTTRSGCER 337
 DB 195 DNPTMTFKEVTCPAELTTRSGCER 218

RESULT 7
 Q9JH95 PRELIMINARY; PRT; 217 AA.
 AC Q9JH95;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045168; BAA98038.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro: IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45.1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 217 AA; 22796 MW; 660DD1346B3769DB CRC64;

Query Match 42.1%; Score 769.5; DB 14; Length 217;
 Best Local Similarity 64.7%; Pred. No. 1.4e-41;
 Matches 132; Conservative 26; Mismatches 41; Indels 3; Gaps 2;

QY 136 SGSTTRVWDCCKASGWPGRASVTGPVDTCAASNGISLLDAN--AOSGCGANGFMCNNNQ 193
 DB 14 SGTTRVWDCCKSGCGWEKKAANDKPIDTCAKQDTRVANSNDTVKSGCDGDFMCYDQT 73
 QY 194 PMAVNDLAVGFAAASAGSNEAGWCCGCELTTSQAASKKRVVQVNTTGGDLGSHNF 253
 DB 74 PMQVSDLSYGFAPAAASAGSNEAGWCCGCELTTSQAASKKRVVQVNTTGGDLGSHNF 132
 QY 254 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCAALPDLQAGCKMRFMPKNS 313
 DB 133 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCAALPDLQAGCKMRFMPKNS 192
 QY 314 DNPTMTFKEVTCPAELTTRSGCER 337
 DB 193 DNPTMTFKEVTCPAELTTRSGCER 216

RESULT 8
 Q9JH83 PRELIMINARY; PRT; 220 AA.
 AC Q9JH83;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";

Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045167; BAA98037.1; -;
DR EMBL; AB045166; BAA98036.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFAF3 CRC64;

Query Match 42.0%; Score 766.5; DB 14; Length 220;
Best Local Similarity 64.2%; Pred. No. 2,1e-41;
Matches 131; Conservative 29; Mismatches 41; Indels 3; Gaps 2;

QY 136 SGGTTRYWDCCKASCSMPGKASVTPVDTCAISNGISLLDAN--AOSGCGNGGEMCNNO 193
DB 17 SGGTTRYWDCCKSGSGWEAKADVSKPLDTCAKDGTTRVANSNDTVKSGDGDGMYCYDQT 76
QY 194 PMAVNDELAYGFAAASINAGSNBAGMCCGCELTFTSGAASGKKMYYQVNTGDLGSNHF 253
DB 77 PMGVNDSYALGFPAALAIISGGEKAA-CCNCEYELFTSGPVNGKMTVQVNTGDLGSNOF 135
QY 254 DLQMPGGVGIFNGCAQOMGAPNDQMGARYGVSSVSDASLPSALOAGCKMRFPNPKNS 313
DB 136 DLAIPEGGVIGIYNGCTAOSGAPADQMSRGVSSSSSCSQLPSGLQAGCCMRPDMQNA 195
QY 314 DNPMTFKEVTCPAELITRSGCER 337
DB 196 DNPSMNFNVVSCSELIAKTCRR 219

RESULT 9

QJUH86 PRELIMINARY; PRT; 219 AA.
AC QJUH86;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN
RP SEQUENCE FROM N.A.
RA Ohkoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045177; BAA98047.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23158 MW; ECD6E6A8ED1D1 CRC64;

Query Match 41.9%; Score 764.5; DB 14; Length 219;
Best Local Similarity 62.7%; Pred. No. 2.8e-41;
Matches 128; Conservative 32; Mismatches 41; Indels 3; Gaps 2;

QY 136 SGGTTRYWDCCKASCSMPGKASVTPVDTCAISNGISLLDAN--AOSGCGNGGEMCNNO 193
DB 16 SGGTTRYWDCCKSGSGWEAKADVSKPLDTCAKDGTTRVANSNDTVKSGDGDGMYCYDQT 75
QY 194 PMAVNDELAYGFAAASINAGSNBAGMCCGCELTFTSGAASGKKMYYQVNTGDLGSNHF 253
DB 76 PMGVNDSYALGFPAALAIISGGEKAA-CCNCEYELFTSGPVNGKMTVQVNTGDLGSNOF 134
QY 254 DLQMPGGVGIFNGCAQOMGAPNDQMGARYGVSSVSDASLPSALOAGCKMRFPNPKNS 313
DB 135 DLAIPEGGVIGIYNGCTAOSGAPADQMSRGVSSSSSCSQLPSGLQAGCCMRPDMQNA 194
QY 314 DNPMTFKEVTCPAELITRSGCER 337
DB 195 DNPSMNFNVVSCSELIAKTCRR 218

RESULT 10

QJUH94 PRELIMINARY; PRT; 221 AA.
AC QJUH94;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN
RP SEQUENCE FROM N.A.
RA Ohkoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045169; BAA98039.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 221 AA; 23220 MW; 8A84CEB0A8C46372 CRC64;

Query Match 41.8%; Score 762.5; DB 14; Length 221;
Best Local Similarity 63.2%; Pred. No. 3.8e-41;
Matches 129; Conservative 34; Mismatches 36; Indels 3; Gaps 2;

QY 136 SGGTTRYWDCCKASCSMPGKASVTPVDTCAISNGISLLDAN--AOSGCGNGGEMCNNO 193
DB 17 SGGTTRYWDCCKSGSGWEAKADVSKPLDTCAKDGTTRVANSNDTVKSGDGDGMYCYDQT 76
QY 194 PMAVNDELAYGFAAASINAGSNBAGMCCGCELTFTSGAASGKKMYYQVNTGDLGSNHF 253
DB 77 PMGVNDSYALGFPAALAIISGGEKAA-CCNCEYELFTSGPVNGKMTVQVNTGDLGSNOF 135
QY 254 DLQMPGGVGIFNGCAQOMGAPNDQMGARYGVSSVSDASLPSALOAGCKMRFPNPKNS 313
DB 136 DLAIPEGGVIGIYNGCTAOSGAPADQMSRGVSSSSSCSQLPSGLQAGCCMRPDMQNA 195
QY 314 DNPMTFKEVTCPAELITRSGCER 337
DB 196 DNPSMNFNVVSCSELIAKTCRR 219

RESULT 11

QJUH86 PRELIMINARY; PRT; 219 AA.
AC QJUH86;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN
RP SEQUENCE FROM N.A.
RA Ohkoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045175; BAA98045.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23030 MW; 179BF1344C6D7024 CRC64;

Query Match 41.6%; Score 759.5; DB 14; Length 219;
Best Local Similarity 62.7%; Pred. No. 5.9e-41;

| | Matches | 128; | Conservative | 31; | Mismatches | 42; | Indels | 3; | Gaps | 2 | |
|----|---------|----------------|--------------|------------|------------|--------|--------------|---------|--------|--------|-----|
| Qy | 136 | SGSTTRRYDDCCKA | SGSGNMPKAS | YTCGPVDTCA | NSIGSLDAN | -A | SGCGNGGNGFMC | NNQ | 193 | | |
| Db | 16 | SGKTRRYDDCCKSG | SGEMKKA | NVDPRIDTCA | DGTTVAAS | NTV | ASGCGGTGYMC | YDPT | 75 | | |
| Qy | 194 | PMAVNDLALYFPA | AAASIGASNEAG | CCGCELTFTT | SGAASG | XKMVQV | VTNTGGD | IGSNHF | 253 | | |
| Db | 76 | PMQVSDSLSTYFPA | AAAACCG | -GESGAC | CCGCELTFTT | SGPNMG | IKMIVQ | INTTGGD | IGSNQF | 134 | |
| Qy | 254 | DLQMPGGGVGI | PNGCAQMGAP | PNDMGARY | GGVSSVSD | CASIP | SALQAC | KRRFPM | FXNS | 313 | |
| Db | 135 | DLAIPGGGVGIY | NGCTSGASGAP | ADMGSR | RYGGVSSR | BEC | SQIP | SGLOAG | CQWR | PMFANA | 194 |
| Qy | 314 | DNPMTPEKAVT | CPAELTTR | SGGER | 337 | | | | | | |
| Db | 195 | DNPINFTNVK | CPSEIIAK | TNCNR | 218 | | | | | | |

| ID | Q9JH93 | PRELIMINARY; | PRT; | 220 AA. |
|--|---|---|------|---------|
| AC | Q9JH93; | | | |
| DT | 01-OCT-2000 (TREMBlrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TREMBlrel. 15, Last sequence update) | | | |
| DT | 01-MAR-2002 (TREMBlrel. 20, Last annotation update) | | | |
| DE | Family 45 cellulase homologue. | | | |
| OS | unclassified eukaryotes. | | | |
| OC | Eukaryota. | | | |
| OX | NCBI_TaxID=42452; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Ohnoko K., Ohkuma M., Moriya S., Kudo T.; | | | |
| RT | "Diverse genes of family 45 cellulase homologues of the symbiotic | | | |
| RT | protists in the hindgut of termite Reticulitermes speratus"; | | | |
| RL | Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases. | | | |
| DR | EMBL; AB045170; BAA98040.1; -. | | | |
| DR | HSSP; P43316; 2ENG. | | | |
| DR | InterPro; IPR000334; GH_45. | | | |
| DR | Pfam; PF02015; Glyco_hydro_45; 1. | | | |
| DR | PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1. | | | |
| SQ | SEQUENCE 220 AA; 23091 MW; 35F174F879C2D65 CRC64; | | | |
| Query Match | 41.4%; Score 755.5; DB 14; Length 220; | | | |
| Best Local Similarity | 62.7%; Pred. No. 1.1e-40; | | | |
| Matches 128; Conservative 31; Mismatches 42; Indels 3; Gaps 2; | | | | |
| QY | 136 | SGSTTRRYDDCKKASGSGWPKASVYGPVDTCAISNGISLIDAN--NDSGCGNGGGMENNNQ | 193 | |
| DB | 17 | TGRTTRRYDDCKKSGSGMEKKAANDPRIDICADGTRVAASNDTVKSGDGGGYNCYDOS | 76 | |
| QY | 194 | PMAVNDLALAYGFPAASISAGNEAGCCGCELTFTSGAAGKNAVQVYNTNGDLSNH | 253 | |
| DB | 77 | PMGVNDSPALGFPAALAAVSGESA--CNCYELTFTSGPVGNGKQTVQVYNTNGDLSNQ | 135 | |
| QY | 254 | DLQMPGGVGIPIFGCAQMGAPNDGMGARYGGVSSVSCASIPSLAQAGCKRPFMPTNS | 313 | |
| DB | 136 | DLAIPGGVGVIYNGCTAAGAPADMGSRVGGVSRSECCQLPSGLQAGCQWRFDWFOA | 195 | |
| QY | 314 | DNPTTFEKEVTCRALTLTRSGER | 337 | |
| DB | 196 | DNPSISFNVVSCPSLTIKTCRR | 219 | |
| RESULT 13 | | | | |
| Q9JH85 | | | | |
| ID | Q9JH85 | PRELIMINARY; | PRT; | 218 AA. |
| AC | Q9JH85; | | | |
| DT | 01-OCT-2000 (TREMBlrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TREMBlrel. 15, Last sequence update) | | | |
| DT | 01-MAR-2002 (TREMBlrel. 20, Last annotation update) | | | |
| DE | Family 45 cellulase homologue. | | | |
| OS | unclassified eukaryotes. | | | |

OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite *Reticulitermes speratus*.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB045178; BAA98048.1; -.
DR HSSP; P43316; JENG.
DR InterPro; IPR000334; GH_45. .
DR Pfam; PF02015; GLYCO_HYDRO_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_P45; UNKNOWN 1.
SQ SEQUENCE 218 AA; 22680 MM; A600FFSB990ADJ3 CRC64;

| | | | | | |
|----|-----------------------|--|--------------------|--------|----------------------------------|
| | Query Match | 41.1%; | Score 750; | DB 14; | Length 218; |
| | Best Local Similarity | 63.1%; | Pred. No. 2,38-40; | | |
| | Matches | 128; | Conservative | 34; | Mismatches 39; Indels 2; Gaps 2; |
| Oy | 137 | GSTRRYWDCCKACSMFPQKASVTGPVDTTCASNIGISLIDANNAQSGC-NGANGFMCNNOPW | 195 | | |
| | | : | : | : | : |
| Db | 17 | GRTRRYWDCCGSGGMFGDKASVSXPDVTCAKDGTTRTAVATSAKSAACDSGGTYMVCYDQTPR | 76 | | |
| | | : | : | : | : |
| Oy | 196 | AVNDELAYGFPAASAIIAGSNENAGGCCGYCELFTFTSGAAGSKGWQVQNTGTGDLGSNHFDL | 255 | | |
| | | : | : | : | : |
| Db | 77 | AVNDSTIYAIQFAAAAVSAGEKKA-CCTCYELFTFTSPVNGKKMTYQVNTINTGDDLSSNQPDI | 135 | | |
| | | : | : | : | : |
| Oy | 256 | OMPGGVGIENGCAAOQCAPNDGNGARVGYSVSDCASLPALQACKKMFNMFKUSND | 315 | | |
| | | : | : | : | : |
| Db | 136 | AIPGGGVGLNYGCTSGOSGAPADGWSRGVSSRECSQLPSGLQAGQMPWFDFWFOAND | 195 | | |
| | | : | : | : | : |
| Oy | 316 | PTMTFEKTECPABLLTTRSQCRRK | 338 | | |
| | | : | : | : | : |
| Db | 196 | PSITFNEVSCPGDILTSTKNCRQ | 218 | | |

| ID | Q9JH96 | PRELIMINARY; | PRT; | 220 AA. |
|----|---|------------------|--------------------|--------------------|
| AC | Q9JH96; | | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Last annotation update) | | | |
| DE | Family 45 cellulase homologue. | | | |
| OS | unclassified eukaryotes. | | | |
| OC | Eukaryota. | | | |
| OX | NCBI_TaxID=42452; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Ohtoko K., Ohkuma M., Moriya S., Kudo T.; | | | |
| RT | "Diverse genes of Family 45 cellulase homologues of the symbiotic | | | |
| RT | protists in the hindgut of termite Reticulitermes speratus."; | | | |
| RL | Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AB045165; BAA98035.1; - | | | |
| DR | HSSP; P43316; 2ENG. | | | |
| DR | InterPro; IPR000334; GH_45. | | | |
| DR | Pfam; PF02015; Glyco_hydro_45; 1. | | | |
| DR | PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1: | | | |
| DR | SEQUENCE 220 AA; 23148 MW; 4F0652F8E8026955 CRC64; | | | |
| QY | Query Match | 40.8%; | Score 745.5; | DB 14; Length 220; |
| QY | Best Local Similarity | 63.7%; | Pred. No. 4.5e-40; | |
| QY | Matches 130; | Conservative 27; | Mismatches 44; | Indels 3; Gaps 2; |
| Db | 136 SGRITRWYDDCKKASCSMGKASVYTPVDTCSASNGISLIDAN--AOSGCGNGGFMCKNNQ | 193 | | |
| Db | 17 SGRITRWYDDCKKSGCKGAEKADVSKPIDTCKADGTRVYASNDPYVYSGCDGEGEYCYDQT | 76 | | |
| QY | 194 PWANVDLAVGFAPAAASITAGSNEAQMCCGVELEFTSGAASGRKRVVYVNTNCGDLGSNHF | 253 | | |
| Db | 77 PRAYNDVSLVGFAPAAASITAGSNEAQMCCGVELEFTSGAASGRKRVVYVNTNCGDLGSNHF | 135 | | |
| QY | 254 DLQMPGGGVGIFNGSCAAQMGAPNDMGARVGVSSVSDCALPSALDAQCKWRPNWPFNS | 313 | | |

Db 136 DIAIPGGVGIYNGTAAOSGAPADWGSRYGVSSRSRCSQLPSGLQAGCOMRPFDMFONA 195
OY 314 DNEPTMTFKEVTCPAELTTRSGCER 337
Db 196 DNPSINFNVSCPGELIANTNCRR 219

RESULT 15

ID 093782 PRELIMINARY; PRT: 305 AA.
AC 093782;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Endoglucanase.
GN EGI.3.
OS Humicola grisea var. thermoides.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_Taxid=5528;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP09854;
RX MEDLINE=99144540; PubMed=9990729;
RA Takashima S., Iikura H., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT "Comparison of gene structures and enzymatic properties between two
endoglucanases from Humicola grisea.";
RL J. Biotechnol. 67:85-97(1999).
DR EMBL; AB003107; BAA74956.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF00734; CBM_1; 1.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR ProDom; PD001821; CBD_fungal; 1.
DR SMART; SM00236; fCBD_1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
SQ SEQUENCE 305 AA; 32174 MW; 28C979D6EDCD771D CRC64;

Query Match

Best local similarity 39.3%; Score 718; DB 3; Length 305;
Matches 127; Conservative 26; Mismatches 47; Indels 6; Gaps 3;

OY 134 SSGSSTRYWDCCKASCSMPGASVYGPVDTCAASNGISLIDANAOSGN-GANGFMNNN 192
Db 21 AADGKSTRYWDCCCKSCGAKKAPVNDVFSNANFORLTFDAKSGCEPGVAVSCADQ 80
OY 193 QPAAVNDDELAYGPAALSTAGSNEAGMCCGCELTFTSGAASGKKWVQVTNTGDLGSH 252
Db 81 TPAAVNDDELAYGPAALSTAGSNEAGMCCGCELTFTSGPAAKKWVQSTISGDLGSH 140
OY 253 FDIQMPGGVGIYNGTAAQWGA-PNDGMAHYGVSSVSDCASLPALQAGCKRFRNMF 311
Db 141 FDIINIPGGVGIYNGTAAQWGA-PNDGMAHYGVSSVSDCASLPALQAGCKRFRNMF 196
OY 312 NSDNPMTFKEVTCPAELTTRSGCER 337
Db 197 NADNPSFSPFQVCCPAELVARTGCR 222

Search completed: June 18, 2003, 17:14:25
Job time : 29.3382 secs